

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga
Guegler, Karl J.
Lal, Preeti

(ii) TITLE OF THE INVENTION: SH3-CONTAINING PROTEINS

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0419 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRAITUT03
(B) CLONE: 865744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Lys Arg Thr Val Ser Asp Asn Ser Leu Ser Asn Ser Arg Gly Glu
  1                               10          15
Gly Lys Pro Asp Leu Lys Phe Gly Gly Lys Ser Lys Gly Lys Leu Trp
  20          25          30
Pro Phe Ile Lys Lys Asn Lys Gly Ala Thr Pro Glu Asp Phe Ser Asn
  35          40          45
Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val Asp Glu
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50	55	60
Leu Asn Lys Glu Ile Gln	Lys Glu Met Asp Gln	Arg Asp Ala Ile Thr
65	70	75
Lys Met Lys Asp Val Tyr	Leu Lys Asn Pro Gln	Met Gly Asp Pro Ala
85	90	95
Ser Leu Asp His Lys	Leu Ala Glu Val Ser	Gln Asn Ile Glu Lys Leu
100	105	110
Arg Val Glu Thr Gln	Lys Phe Glu Ala Trp	Leu Ala Glu Val Glu Gly
115	120	125
Arg Leu Pro Ala Arg	Asn Glu Gln Ala Arg	Arg Gln Ser Gly Leu Tyr
130	135	140
Asp Ser Gln Asn Pro	Pro Thr Val Asn Asn Cys	Ala Gln Asp Arg Glu
145	150	155
Ser Pro Asp Gly Ser	Tyr Thr Glu Glu Gln	Ser Gln Glu Ser Glu Met
165	170	175
Lys Val Leu Ala Thr	Asp Phe Asp Asp Glu Glu	Pro
180	185	190
Leu Pro Ala Ile Gly	Thr Cys Lys Ala Leu	Tyr Thr Phe Glu Gly Gln
195	200	205
Asn Glu Gly Thr Ile	Ser Val Val Glu Gly	Glu Thr Leu Tyr Val Ile
210	215	220
Glu Glu Asp Lys Gly	Asp Gly Trp Thr Arg	Ile Arg Arg Asn Glu Asp
225	230	235
Glu Glu Gly Tyr Val	Pro Thr Ser Tyr Val	Glu Val Cys Leu Asp Lys
245	250	255
Asn Ala Lys Gly Ala	Lys Thr Tyr Ile	
260	265	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT03
 (B) CLONE: 865744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGTAAAAGCA	GCCGAATCAA	TTGATCAGAA	AAATGATTCA	CAGCTGGTAA	TAGAAGCTTA	60
TAAATCAGGG	TTTGAGCCTC	CTGGAGACAT	TGAATTTGAG	GATTACACTC	AGCCAATGAA	120
GCGCACTGTG	TCAGATAACA	GCCTTTCAAA	TTCCAGAGGA	GAAGGCAAAAC	CAGACCTCAA	180
ATTTGTTGGC	AAATCCAAAG	GAAAGTTATG	GCCGTTCATC	AAAAAAATA	AGGGTGCAAC	240
ACCGGAGAT	TTCAGCAACC	TCCCACCTGA	ACAAAGGAAGG	AAAAAGCTGC	AGCAGAAAGT	300
CGATGAGTTA	AATAAAGAAA	TTCAGAAGGA	GATGGATCAA	AGAGATGCCA	TAACAAAAAT	360
GAAAGATGTC	TACCTAAAGA	ATCCTCAGAT	GGGAGACCCA	GCCAGTTTGG	ATCACAAAT	420
AGCAGAAGTC	AGCCAAAATA	TAGAGAAACT	GCGAGTAGAG	ACCCAGAAAT	TTGAGGCCCTG	480
GCTGGCTGAG	GTTGAAGGCC	GGCTCCCAGC	ACGCAACGAG	CAGGCGCGCC	GGCAGAGCCG	540
ACTGTACGAC	AGCCAGAACC	CACCCACAGT	CAACAACATG	GCCCAGGACC	GTGAGAGCCC	600
AGATGGCAGT	TACACAGAGG	AGCAGAGTCA	GGAGAGTAG	ATGAAGTGC	TGCGCCACGA	660
TTTTTACGAC	GAGTTTGATG	ATGAGGAGCC	CCTCCCTGCC	ATAGGACGCT	GCAAAAGCTCT	720
CTACACATTT	GAAGGTCAGA	ATGAAGGAAC	GATTTCCGTA	GTTGAAGGAG	AAACATTGTA	780
TGTCATAGAG	GAAGACAAGG	GCGATGGCTG	GACCCGCATT	CGAGAAAATG	AAGATGAAGA	840
GGGTTATGTC	CCCACTTCAT	ATGTCGAAGT	CTGTTTGGAC	AAAAATGCCA	AAGGTGCTAA	900
GACTTATATT	TAAATACCATA	AAAAAAATA	ACTTAAAAAA	AATGGAGTTG	TTTCTCCCCA	960
CAACCGTGAC	TGTTACAGCG	AGTTCCCTCA	GAGACTGGCT	GGCAAGCACC	ATTAATGCACG	1020
TTCTCCTGTA	GTCTCAGTGC	GACTTCAGGG	TCCGGGCACC	TGAATTGCTC	TGTCATGTTT	1080
GGGCTGTAA	CAGTTTTCAC	TTGCTGATGA	AATTTTATGT	GGAAAAGCTGC	CAACCCGCCAA	1140
CTTACAGTCA	TGTCATTCAA	AATCTGATAA	ACATTTCTTC	TTTTGGCGGT	ACTCTGTAGAT	1200
TAAAAAAA	GTTCATTGTT	AGCTTCTCAT	CTTTCTGAAT	TTAAAGGCGG	GCACGCATCA	1260
TGCAAGTGCC	AAAGACTTCC	CTACTTTTGT	TTATATCTAG	TATCCACCAT	ACACTGAGCT	1320
ACATAGTGTG	GTTCAGATT	GTAACCTAAT	AAACTGAAC	GTGTTAGTTT	GTAAAAATGG	1380
ATACTCATTC	ACTTGGGGAG	GAGTCACAAG	TGAAATACCA	TCTCTTTCTT	GACTAAAGCG	1440

GTAAATAAGG TTCTTATTG

1459

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
 (B) CLONE: 1816529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Asp Val Tyr Glu Lys Thr Pro Gln Met Gly Asp Pro Ala Ser
 1 5 10 15
 Leu Glu Pro Gln Ile Ala Glu Thr Leu Ser Asn Ile Glu Arg Leu Lys
 20 25 30
 Leu Glu Val Gln Lys Tyr Glu Ala Trp Leu Ala Glu Ala Glu Ser Arg
 35 40 45
 Val Leu Ser Asn Arg Gly Asp Ser Leu Ser Arg His Ala Arg Pro Pro
 50 55 60
 Xaa Pro Pro Ala Ser Ala Pro Pro Asp Ser Ser Ser Asn Ser Ala Ser
 65 70 75 80
 Gln Asp Thr Lys Glu Ser Ser Glu Glu Pro Pro Ser Glu Glu Ser Gln
 85 90 95
 Asp Thr Pro Ile Tyr Thr Glu Phe Asp Glu Asp Phe Glu Glu Glu Pro
 100 105 110
 Thr Ser Pro Ile Gly His Cys Val Ala Ile Tyr His Phe Glu Gly Ser
 115 120 125
 Ser Glu Gly Thr Ile Ser Met Ala Glu Gly Glu Asp Leu Ser Leu Met
 130 135 140
 Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Val Arg Arg Lys Glu Gly
 145 150 155 160
 Gly Glu Gly Tyr Val Pro Thr Ser Tyr Leu Arg Val Thr Leu Asn
 165 170 175

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
 (B) CLONE: 1816529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAACCGTG CACCCCTNCGA CAGCAGTCTG GGCACCCCTT ACGGATGGAC GGNCTGAACT 60
 CCGAGGNCGG GGTGCGACGG GCACCAAGCG CTGGNCTTTT GGCAAGAAGA ACAAGACAGT 120
 GGTGACCGAG GATTTTAGCC ACTTGCCCCC AGAGCAGCAG CGAAACACGG TTCAACAGCA 180
 GTTGGAAGAA CGCAGTGTG AACTTCAGAA GGAGGTTGAC CAGAGGGAAG CCCTAAAGAA 240
 AATGAAGGAT GTCTATGAGA AGACACCTCA GATGCGGGAC CCCGCCAGCT TGGAGCCCCA 300
 GATCGTTGAA ACCCTGAGCA ACATTGAAAG GCTGAAATTG GAAGTGCAGA AGTATGAGGC 360
 GTGGCTGGCA GAAGCTGAAA GTGCGATCCT TAGCAACCGG GGAGACAGCC TGAGCCGGCA 420
 CGCCCGGCTT CCGGACCC CCGCTAGCGC CCCGCCAGAC AGCAGCAGCA ACAGCCCATC 480
 ACAGGACACC AAGGAGAGCT CTGAAGAGCC TCCCTCAGAA GAGAGCCGAG ACACCCCATC 540
 TTACACCGAG TTTGATGAG ATTTTCGAGGA GGAACCCACA TCCCCCATAG GTCACTGTGT 600
 GGCCATCTAC CACTTTGAGG GGTCCAGCGA GGGCACTATC TCTATGGCCG AGGGTGAAGA 660
 CCTCAGCTTT ATGGAAGAAG ACAAGGGGGA CGGGTGGACC CGGGTCAGGC GGAAAGAGGG 720
 AGGCGAGGGC TACGTGCCCA CCTCTACCT CCGAGTCAGC CTCAATTGAA CCC 773

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1255033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Ile His Cys Phe Arg Ser Leu Lys Arg Gly Gly Val Thr Pro Glu
 1 5 10 15
 Asp Phe Ser Asn Phe Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln
 20 25 30
 Lys Val Asp Asp Leu Asn Arg Glu Ile Gln Lys Glu Thr Asp Gln Arg
 35 40 45
 Asp Ala Ile Thr Lys Met Lys Asp Val Tyr Leu Lys Asn Pro Gln Met
 50 55 60
 Gly Asp Pro Ala Ser Leu Asp Gln Lys Leu Thr Glu Val Thr Gln Asn
 65 70 75 80
 Ile Glu Lys Leu Arg Leu Glu Ala Gln Lys Phe Glu Ala Trp Leu Ala
 85 90 95
 Glu Val Glu Gly Arg Leu Pro Ala Arg Ser Glu Gln Ala Arg Arg Gln
 100 105 110
 Ser Gly Leu Tyr Asp Gly Gln Thr His Gln Thr Val Thr Asn Cys Ala
 115 120 125
 Gln Asp Arg Glu Ser Pro Asp Gly Ser Tyr Thr Glu Glu Gln Ser Gln
 130 135 140
 Glu Ser Glu His Lys Val Leu Ala Pro Asp Phe Asp Asp Glu Phe Asp
 145 150 155 160
 Asp Glu Glu Pro Leu Pro Ala Ile Gly Thr Cys Lys Ala Leu Tyr Thr
 165 170 175
 Phe Glu Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu Gly Glu Thr
 180 185 190
 Leu Ser Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ile Arg
 195 200 205
 Arg Asn Glu Asp Glu Glu Gly Tyr Phe Pro Thr Ser Tyr Val Glu Val
 210 215 220
 Tyr Leu Asp Lys Asn Ala Lys Gly Ala Lys Thr Tyr Ile
 225 230 235